

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/518,283

Source: P4719

Date Processed by STIC: 12/28/04

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PCT

RAW SEQUENCE LISTING

DATE: 12/28/2004

PATENT APPLICATION: US/10/518,283

TIME: 11:44:26

Input Set : D:\Ispt1012.txt

Output Set: N:\CRF4\12282004\J518283.raw

4 <110> APPLICANT: Bennett, Clarence Frank
 5 Freier, Suan M.
 6 Dobie, Kenneth W.
 8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION
 10 <130> FILE REFERENCE: ISPT-1012
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/518,283
 C--> 12 <141> CURRENT FILING DATE: 2004-12-16
 12 <150> PRIOR APPLICATION NUMBER: PCT/US03/18923
 13 <151> PRIOR FILING DATE: 2003-06-17
 15 <150> PRIOR APPLICATION NUMBER: US 10/174,014
 16 <151> PRIOR FILING DATE: 2002-06-17
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 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 29 <223> OTHER INFORMATION: Antisense Oligonucleotide
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 51 <213> ORGANISM: Artificial Sequence
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 62 <211> LENGTH: 8686
 63 <212> TYPE: DNA
 64 <213> ORGANISM: H. sapiens
 66 <220> FEATURE:
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ppr 6-7

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75 gggcctggga gcagctcccc gccgaccccc accacc atg tcg ggc tcc aca cag      174
76                                     Met Ser Gly Ser Thr Gln
77                                     1           5
78 cct gtg gca cag acg tgg agg gcc act gag ccc cgc tac ccg ccc cac      222
79 Pro Val Ala Gln Thr Trp Arg Ala Thr Glu Pro Arg Tyr Pro Pro His
80               10               15               20
81 agc ctt tcc tac cca gtg cag atc gcc cgg acg cac acg gac gtc ggg      270
82 Ser Leu Ser Tyr Pro Val Gln Ile Ala Arg Thr His Thr Asp Val Gly
83               25               30               35
84 ctc ctg gag tac cag cac cac tcc cgc gac tat gcc tcc cac ctg tcg      318
85 Leu Leu Glu Tyr Gln His His Ser Arg Asp Tyr Ala Ser His Leu Ser
86               40               45               50
87 ccc ggc tcc atc atc cag ccc cag cgg cgg agg ccc tcc ctg ctg tct      366
88 Pro Gly Ser Ile Ile Gln Pro Gln Arg Arg Arg Pro Ser Leu Leu Ser
89 55               60               65               70
90 gag ttc cag ccc ggg aat gaa cgg tcc cag gag ctc cac ctg cgg cca      414
91 Glu Phe Gln Pro Gly Asn Glu Arg Ser Gln Glu Leu His Leu Arg Pro
92               75               80               85
93 gag tcc cac tca tac ctg ccc gag ctg ggg aag tca gag atg gag ttc      462
94 Glu Ser His Ser Tyr Leu Pro Glu Leu Gly Lys Ser Glu Met Glu Phe
95               90               95               100
96 att gaa agc aag cgc cct cgg cta gag ctg ctg cct gac ccc ctg ctg      510
97 Ile Glu Ser Lys Arg Pro Arg Leu Glu Leu Leu Pro Asp Pro Leu Leu
98               105               110               115
99 cga ccg tca ccc ctg ctg gcc acg ggc cag cct gcg gga tct gaa gac      558
100 Arg Pro Ser Pro Leu Leu Ala Thr Gly Gln Pro Ala Gly Ser Glu Asp
101               120               125               130
102 ctc acc aag gac cgt agc ctg acg ggc aag ctg gaa ccg gtg tct ccc      606
103 Leu Thr Lys Asp Arg Ser Leu Thr Gly Lys Leu Glu Pro Val Ser Pro
104 135               140               145               150
105 ccc agc ccc ccg cac act gac cct gag ctg gag ctg gtg ccg cca cgg      654
106 Pro Ser Pro Pro His Thr Asp Pro Glu Leu Glu Leu Val Pro Pro Arg
107               155               160               165
108 ctg tcc aag gag gag ctg atc cag aac atg gac cgc gtg gac cga gag      702
109 Leu Ser Lys Glu Glu Leu Ile Gln Asn Met Asp Arg Val Asp Arg Glu
110               170               175               180
111 atc acc atg gta gag cag cag atc tct aag ctg aag aag aag cag caa      750
112 Ile Thr Met Val Glu Gln Gln Ile Ser Lys Leu Lys Lys Lys Gln Gln
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114 cag ctg gag gag gag gct gcc aag ccg ccc gag cct gag aag ccc gtg      798
115 Gln Leu Glu Glu Glu Ala Ala Lys Pro Pro Glu Pro Glu Lys Pro Val
116               200               205               210
117 tca ccg ccg ccc atc gag tcg aag cac cgc agc ctg gtg cag atc atc      846
118 Ser Pro Pro Pro Ile Glu Ser Lys His Arg Ser Leu Val Gln Ile Ile

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122				235			240	
123	ggc	ctg	ggg	ccc	cag	gtg	gag	ctg
124	Gly	Leu	Gly	Pro	Gln	Val	Glu	Leu
125			250				255	
126	acc	cgg	cag	tat	cat	gag	aac	atc
127	Thr	Arg	Gln	Tyr	His	Glu	Asn	Ile
128			265				270	
129	aag	cta	atc	ttg	tac	ttc	aag	agg
130	Lys	Leu	Ile	Leu	Tyr	Phe	Lys	Arg
131		280					285	
132	gag	cag	aag	ttc	tgc	cag	cgc	tat
133	Glu	Gln	Lys	Phe	Cys	Gln	Arg	Tyr
134	295						300	
135	aag	aag	gtg	gag	cgc	atc	gag	aac
136	Lys	Lys	Val	Glu	Arg	Ile	Glu	Asn
137							315	
138	agc	aag	gtt	cgc	gag	tac	tac	gag
139	Ser	Lys	Val	Arg	Glu	Tyr	Tyr	Glu
140			330				335	
141	cag	cgc	gag	ctg	cag	gag	cgc	atg
142	Gln	Arg	Glu	Leu	Gln	Glu	Arg	Met
143			345				350	
144	ggg	ctg	tcc	atg	tcg	ccc	gcc	cgc
145	Gly	Leu	Ser	Met	Ser	Pro	Ala	Arg
146		360					365	
147	atc	gat	ggc	ctc	tca	gag	cag	gag
148	Ile	Asp	Gly	Leu	Ser	Glu	Gln	Glu
149	375						380	
150	ctg	gcc	gtg	atc	ccg	ccc	atg	ctg
151	Leu	Ala	Val	Ile	Pro	Pro	Met	Leu
152							395	
153	aag	ttc	atc	aac	atg	aac	ggg	ctt
154	Lys	Phe	Ile	Asn	Met	Asn	Gly	Leu
155							410	
156	aaa	gac	cgc	cag	gtc	atg	aac	atg
157	Lys	Asp	Arg	Gln	Val	Met	Asn	Met
158			425				430	
159	ttc	cgg	gag	aag	ttc	atg	cag	cat
160	Phe	Arg	Glu	Lys	Phe	Met	Gln	His
161		440					445	
162	tca	ttc	ctg	gag	agg	aag	aca	gtg
163	Ser	Phe	Leu	Glu	Arg	Lys	Thr	Val
164	455						460	
165	ctg	act	aag	aag	aat	gag	aac	tat
166	Leu	Thr	Lys	Lys	Asn	Glu	Asn	Tyr
167							475	

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169	Arg	Arg	Arg	Gly	Lys	Ser	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
170				490					495						500		
171	cag	cag	cag	cag	cag	cag	cag	ccc	atg	ccc	cgc	agc	agc	cag	gag	gag	1710
172	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Met	Pro	Arg	Ser	Ser	Gln	Glu	Glu	
173				505				510						515			
174	aaa	gat	gag	aag	gag	aag	gaa	aag	gag	gcg	gag	aag	gag	gag	gag	aag	1758
175	Lys	Asp	Glu	Lys	Glu	Lys	Glu	Lys	Glu	Ala	Glu	Lys	Glu	Glu	Glu	Lys	
176				520				525						530			
177	ccg	gag	gtg	gag	aac	gac	aag	gaa	gac	ctc	ctc	aag	gag	aag	aca	gac	1806
178	Pro	Glu	Val	Glu	Asn	Asp	Lys	Glu	Asp	Leu	Leu	Lys	Glu	Lys	Thr	Asp	
179	535						540							545		550	
180	gac	acc	tca	ggg	gag	gac	aac	gac	gag	aag	gag	gct	gtg	gcc	tcc	aaa	1854
181	Asp	Thr	Ser	Gly	Glu	Asp	Asn	Asp	Glu	Lys	Glu	Ala	Val	Ala	Ser	Lys	
182				555										560		565	
183	ggc	cgc	aaa	act	gcc	aac	agc	cag	gga	aga	cgc	aaa	ggc	cgc	atc	acc	1902
184	Gly	Arg	Lys	Thr	Ala	Asn	Ser	Gln	Gly	Arg	Arg	Lys	Gly	Arg	Ile	Thr	
185				570										575		580	
186	cgc	tca	atg	gct	aat	gag	gcc	aac	agc	gag	gag	gcc	atc	acc	ccc	cag	1950
187	Arg	Ser	Met	Ala	Asn	Glu	Ala	Asn	Ser	Glu	Glu	Ala	Ile	Thr	Pro	Gln	
188				585				590						595			
189	cag	agc	gcc	gag	ctg	gcc	tcc	atg	gag	ctg	aat	gag	agt	tct	cgc	tgg	1998
190	Gln	Ser	Ala	Glu	Leu	Ala	Ser	Met	Glu	Leu	Asn	Glu	Ser	Ser	Arg	Trp	
191				600				605						610			
192	aca	gaa	gaa	gaa	atg	gaa	aca	gcc	aag	aaa	ggt	ctc	ctg	gaa	cac	ggc	2046
193	Thr	Glu	Glu	Glu	Met	Glu	Thr	Ala	Lys	Lys	Gly	Leu	Leu	Glu	His	Gly	
194	615							620						625		630	
195	cgc	aac	tgg	tcg	gcc	atc	gcc	cgg	atg	gtg	ggc	tcc	aag	act	gtg	tcg	2094
196	Arg	Asn	Trp	Ser	Ala	Ile	Ala	Arg	Met	Val	Gly	Ser	Lys	Thr	Val	Ser	
197				635										640		645	
198	cag	tgt	aag	aac	ttc	tac	ttc	aac	tac	aag	aag	agg	cag	aac	ctc	gat	2142
199	Gln	Cys	Lys	Asn	Phe	Tyr	Phe	Asn	Tyr	Lys	Lys	Arg	Gln	Asn	Leu	Asp	
200				650										655		660	
201	gag	atc	ttg	cag	cag	cac	aag	ctg	aag	atg	gag	aag	gag	agg	aac	gcg	2190
202	Glu	Ile	Leu	Gln	Gln	His	Lys	Leu	Lys	Met	Glu	Lys	Glu	Arg	Asn	Ala	
203				665										670		675	
204	cgg	agg	aag	aag	aag	aaa	gcg	ccg	gcg	gcg	gcc	agc	gag	gag	gct	gca	2238
205	Arg	Arg	Lys	Lys	Lys	Lys	Ala	Pro	Ala	Ala	Ala	Ser	Glu	Glu	Ala	Ala	
206				680				685						690			
207	ttc	ccg	ccc	gtg	gtg	gag	gat	gag	gag	atg	gag	gcg	tcg	ggc	gtg	acg	2286
208	Phe	Pro	Pro	Val	Val	Glu	Asp	Glu	Glu	Met	Glu	Ala	Ser	Gly	Val	Thr	
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211	Gly	Asn	Glu	Glu	Glu	Met	Val	Glu	Glu	Ala	Glu	Ala	Thr	Val	Asn	Asn	
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213	agc	tca	gac	acc	gag	agc	atc	ccc	tct	cct	cac	act	gag	gcc	gcc	aag	2382
214	Ser	Ser	Asp	Thr	Glu	Ser	Ile	Pro	Ser	Pro	His	Thr	Glu	Ala	Ala	Lys	
215				730										735		740	
216	gac	aca	ggg	cag	aat	ggg	ccc	aag	ccc	cca	gcc	acc	ctg	ggc	gcc	gac	2430

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220	Gly	Pro	Pro	Pro	Gly	Pro	Pro	Thr	Pro	Pro	Pro	Glu	Asp	Ile	Pro	Ala	
221			760					765					770				
222	ccc	act	gag	tcc	acc	ccg	gcc	tct	gaa	gcc	acc	tta	gcc	cct	acg	ccc	2526
223	Pro	Thr	Glu	Ser	Thr	Pro	Ala	Ser	Glu	Ala	Thr	Leu	Ala	Pro	Thr	Pro	
224			775					780					785			790	
225	cca	cca	gca	ccc	cca	ttt	ccc	tct	tca	cct	cct	cct	gtg	gtc	ccc	aag	2574
226	Pro	Pro	Ala	Pro	Pro	Phe	Pro	Ser	Ser	Pro	Pro	Pro	Val	Val	Pro	Lys	
227						795					800				805		
228	gag	gag	aag	gag	gag	gag	acc	gca	gca	gcg	ccc	cca	gtg	gag	gag	ggg	2622
229	Glu	Glu	Lys	Glu	Glu	Glu	Thr	Ala	Ala	Ala	Pro	Pro	Val	Glu	Glu	Gly	
230				810						815				820			
231	gag	gag	cag	aag	ccc	ccc	gcg	gct	gag	gag	ctg	gca	gtg	gac	aca	ggg	2670
232	Glu	Glu	Gln	Lys	Pro	Pro	Ala	Ala	Glu	Glu	Leu	Ala	Val	Asp	Thr	Gly	
233			825					830					835				
234	aag	gcc	gag	gag	ccc	gtc	aag	agc	gag	tgc	acg	gag	gaa	gcc	gag	gag	2718
235	Lys	Ala	Glu	Glu	Pro	Val	Lys	Ser	Glu	Cys	Thr	Glu	Glu	Ala	Glu	Glu	
236			840					845					850				
237	ggg	ccg	gcc	aag	ggc	aag	gac	gcg	gag	gcc	gct	gag	gcc	acg	gcc	gag	2766
238	Gly	Pro	Ala	Lys	Gly	Lys	Asp	Ala	Glu	Ala	Ala	Glu	Ala	Thr	Ala	Glu	
239						860					865				870		
240	agg	gcg	ctc	aag	gca	gag	aag	aag	gag	ggc	ggg	agc	ggc	agg	gcc	acc	2814
241	Arg	Ala	Leu	Lys	Ala	Glu	Lys	Lys	Glu	Gly	Gly	Ser	Gly	Arg	Ala	Thr	
242						875					880				885		
243	aca	gcc	aag	agc	tcg	ggc	gcc	ccc	cag	gac	agc	gac	tcc	agt	gcc	acc	2862
244	Thr	Ala	Lys	Ser	Ser	Gly	Ala	Pro	Gln	Asp	Ser	Asp	Ser	Ser	Ala	Thr	
245						890					895			900			
246	tgc	agt	gca	gac	gag	gtg	gat	gag	gcc	gag	ggc	ggc	gac	aag	aac	cgg	2910
247	Cys	Ser	Ala	Asp	Glu	Val	Asp	Glu	Ala	Glu	Gly	Gly	Asp	Lys	Asn	Arg	
248			905					910					915				
249	ctg	ctg	tcc	cca	agg	ccc	agc	ctc	ctc	acc	ccg	act	ggc	gac	ccc	cgg	2958
250	Leu	Leu	Ser	Pro	Arg	Pro	Ser	Leu	Leu	Thr	Pro	Thr	Gly	Asp	Pro	Arg	
251			920					925					930				
252	gcc	aat	gcc	tca	ccc	cag	aag	cca	ctg	gac	ctg	aag	cag	ctg	aag	cag	3006
253	Ala	Asn	Ala	Ser	Pro	Gln	Lys	Pro	Leu	Asp	Leu	Lys	Gln	Leu	Lys	Gln	
254			935				940				945				950		
255	cga	gcg	gct	gcc	atc	ccc	ccc	atc	cag	gtc	acc	aaa	gtc	cat	gag	ccc	3054
256	Arg	Ala	Ala	Ala	Ile	Pro	Pro	Ile	Gln	Val	Thr	Lys	Val	His	Glu	Pro	
257						955					960				965		
258	ccc	cgg	gag	gac	gca	gct	ccc	acc	aag	cca	gct	ccc	cca	gcc	cca	ccg	3102
259	Pro	Arg	Glu	Asp	Ala	Ala	Pro	Thr	Lys	Pro	Ala	Pro	Pro	Ala	Pro	Pro	
260						970					975				980		
261	cca	ccg	caa	aac	ctg	cag	ccg	gag	agc	gac	gcc	cct	cag	cag	cct	ggc	3150
262	Pro	Pro	Gln	Asn	Leu	Gln	Pro	Glu	Ser	Asp	Ala	Pro	Gln	Gln	Pro	Gly	
263						985					990				995		
264	agc	agc	ccc	cgg	ggc	aag	agc	agg	agc	ccg	gca	ccc	ccc	gcc	gac	aag	3198
265	Ser	Ser	Pro	Arg	Gly	Lys	Ser	Arg	Ser	Pro	Ala	Pro	Pro	Ala	Asp	Lys	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:12; N Pos. 201570,201571,201572,201573,201574,201575,201576,201577
Seq#:12; N Pos. 201578,201579,201580,201581,201582,201583,201584,201585
Seq#:12; N Pos. 201586,201587,201588,201589,201590,201591,201592,201593
Seq#:12; N Pos. 201594,201595,201596,201597,201598,201599,201600,201601
Seq#:12; N Pos. 201602,201603,201604,201605,201606,201607,201608,201609
Seq#:12; N Pos. 201610,201611,201612,201613,201614,201615,201616,201617

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/518,283

DATE: 12/28/2004
TIME: 11:44:27

Input Set : D:\Ispt1012.txt
Output Set: N:\CRF4\12282004\J518283.raw

Seq#:12; N Pos. 201618,201619,201620,201621,201622,201623,201624,201625
Seq#:12; N Pos. 201626,201627,201628,201629,201630,201631,201632,201633
Seq#:12; N Pos. 201634,201635,201636,201637,201638,201639,201640,201641
Seq#:12; N Pos. 201642,201643,201644,201645,201646,201647,201648,201649
Seq#:12; N Pos. 201650,201651,201652,201653,201654,201655,201656,201657
Seq#:12; N Pos. 201658,201659,201660,201661,202839,202840,202841,202842
Seq#:12; N Pos. 202843,202844,202845,202846,202847,202848,202849,202850

VERIFICATION SUMMARY

DATE: 12/28/2004

PATENT APPLICATION: US/10/518,283

TIME: 11:44:27

Input Set : D:\Ispt1012.txt

Output Set: N:\CRF4\12282004\J518283.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1164 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1168 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1176 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1180 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1192 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1196 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1200 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1204 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1208 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1212 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1216 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1220 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1224 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1228 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1232 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1236 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1240 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1248 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1252 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1260 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1264 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1268 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1272 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1276 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1280 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1284 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1288 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1292 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1296 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1300 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1304 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1308 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1312 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1316 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1320 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1324 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1328 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1332 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1336 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1340 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1344 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12

VERIFICATION SUMMARY

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L:1348 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1352 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1356 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1360 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:5308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:77940
M:341 Repeated in SeqNo=12